Sequence Listing

SEQUENCE LISTING

<110> Seikagaku Corporation

<120> Catalyst for cleaving a sugar chain

<130> P04778600

<150> JP 2003-097301
<151> 2003-03-31

<150> JP 2003-113965
<151> 2003-04-18

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<170> PatentIn version 3.1

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<212> DNA
<213> Homo sapiens

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1               5                  10                  15
gat atg gcc caa ggc ttt agg ggc ccc ttg cta ccc aac cgg ccc ttc       96
Asp Met Ala Gln Gly Phe Arg Gly Pro Leu Leu Pro Asn Arg Pro Phe
            20                  25                  30
acc acc gtc tgg aat gca aac acc cag tgg tgc ctg gag agg cac ggt      144
Thr Thr Val Trp Asn Ala Asn Thr Gln Trp Cys Leu Glu Arg His Gly
        35                  40                  45
gtg gac gtg gat gtc agt gtc ttc gat gtg gta gcc aac cca ggg cag      192
Val Asp Val Asp Val Ser Val Phe Asp Val Val Ala Asn Pro Gly Gln
    50                  55                  60
acc ttc cgc ggc cct gac atg aca att ttc tat agc tcc cag ctg ggc      240
Thr Phe Arg Gly Pro Asp Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
65                  70                  75                  80
acc tac ccc tac tac acg ccc act ggg gag cct gtg ttt ggt ggt ctg      288
Thr Tyr Pro Tyr Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu
                85                  90                  95
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ccc cag aat gcc agc ctg att gcc cac ctg gcc cgc aca ttc cag gac      336
Pro Gln Asn Ala Ser Leu Ile Ala His Leu Ala Arg Thr Phe Gln Asp
            100                 105                 110
atc ctg gct gcc ata cct gct cct gac ttc tca ggg ctg gca gtc atc      384
Ile Leu Ala Ala Ile Pro Ala Pro Asp Phe Ser Gly Leu Ala Val Ile
        115                 120                 125
gac tgg gag gca tgg cgc cca cgc tgg gcc ttc aac tgg gac acc aag      432
Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys
    130                 135                 140
gac att tac cgg cag cgc tca cgg gca ctg gta cag gca cag cac cct      480
Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Ala Gln His Pro
145                 150                 155                 160
gat tgg cca gct cct cag gtg gag gca gta gcc cag gac cag ttc cag      528
Asp Trp Pro Ala Pro Gln Val Glu Ala Val Ala Gln Asp Gln Phe Gln
                165                 170                 175
gga gct gca cgg gcc tgg atg gca ggc acc ctc cag ctg ggg cgg gca      576
Gly Ala Ala Arg Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Arg Ala
            180                 185                 190
ctg cgt cct cgc ggc ctc tgg ggc ttc tat ggc ttc cct gac tgc tac      624
Leu Arg Pro Arg Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr
        195                 200                 205
aac tat gac ttt cta agc ccc aac tac acc ggc cag tgc cca tca ggc      672
Asn Tyr Asp Phe Leu Ser Pro Asn Tyr Thr Gly Gln Cys Pro Ser Gly
    210                 215                 220
atc cgt gcc caa aat gac cag cta ggg tgg ctg tgg ggc cag agc cgt      720
Ile Arg Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg
225                 230                 235                 240
gcc ctc tat ccc agc atc tac atg ccc gca gtg ctg gag ggc aca ggg      768
Ala Leu Tyr Pro Ser Ile Tyr Met Pro Ala Val Leu Glu Gly Thr Gly
                245                 250                 255
aag tca cag atg tat gtg caa cac cgt gtg gcc gag gca ttc cgt gtg      816
Lys Ser Gln Met Tyr Val Gln His Arg Val Ala Glu Ala Phe Arg Val
            260                 265                 270
gct gtg gct gct ggt gac ccc aat ctg ccg gtg ctg ccc tat gtc cag      864
Ala Val Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Val Gln
        275                 280                 285
atc ttc tat gac acg aca aac cac ttt ctg ccc ctg gat gag ctg gag      912
Ile Phe Tyr Asp Thr Thr Asn His Phe Leu Pro Leu Asp Glu Leu Glu
    290                 295                 300
cac agc ctg ggg gag agt gcg gcc cag ggg gca gct gga gtg gtg ctc      960
His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu
305                 310                 315                 320
tgg gtg agc tgg gaa aat aca aga acc aag gaa tca tgt cag gcc atc     1008
Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ala Ile
                325                 330                 335
aag gag tat atg gac act aca ctg ggg ccc ttc atc ctg aac gtg acc     1056
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Lys Glu Tyr Met Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr
                340                 345                 350
agt ggg gcc ctt ctc tgc agt caa gcc ctg tgc tcc ggc cat ggc cgc     1104
Ser Gly Ala Leu Leu Cys Ser Gln Ala Leu Cys Ser Gly His Gly Arg
        355                 360                 365
tgt gtc cgc cgc acc agc cac ccc aaa gcc ctc ctc ctc ctt aac cct     1152
Cys Val Arg Arg Thr Ser His Pro Lys Ala Leu Leu Leu Leu Asn Pro
    370                 375                 380
gcc agt ttc tcc atc cag ctc acg cct ggt ggt ggg ccc ctg agc ctg     1200
Ala Ser Phe Ser Ile Gln Leu Thr Pro Gly Gly Gly Pro Leu Ser Leu
385                 390                 395                 400
cgg ggt gcc ctc tca ctt gaa gat cag gca cag atg gct gtg gag ttc     1248
Arg Gly Ala Leu Ser Leu Glu Asp Gln Ala Gln Met Ala Val Glu Phe
                405                 410                 415
aaa tgt cga tgc tac cct ggc tgg cag gca ccg tgg tgt gag cgg aag     1296
Lys Cys Arg Cys Tyr Pro Gly Trp Gln Ala Pro Trp Cys Glu Arg Lys
            420                 425                 430
agc atg tgg tga                                                    1308
Ser Met Trp
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<210> 2
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<212> PRT
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<400> 2

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1               5                   10                  15
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            20                  25                  30
Thr Thr Val Trp Asn Ala Asn Thr Gln Trp Cys Leu Glu Arg His Gly
        35                  40                  45
Val Asp Val Asp Val Ser Val Phe Asp Val Val Ala Asn Pro Gly Gln
    50                  55                  60
Thr Phe Arg Gly Pro Asp Met Thr Ile Phe Tyr Ser Ser Gln Leu Gly
65                  70                  75                  80
Thr Tyr Pro Tyr Tyr Thr Pro Thr Gly Glu Pro Val Phe Gly Gly Leu
                85                  90                  95
Pro Gln Asn Ala Ser Leu Ile Ala His Leu Ala Arg Thr Phe Gln Asp
            100                 105                 110
Ile Leu Ala Ala Ile Pro Ala Pro Asp Phe Ser Gly Leu Ala Val Ile
        115                 120                 125
Asp Trp Glu Ala Trp Arg Pro Arg Trp Ala Phe Asn Trp Asp Thr Lys
    130                 135                 140
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Asp Ile Tyr Arg Gln Arg Ser Arg Ala Leu Val Gln Ala Gln His Pro
145                 150                 155                 160
Asp Trp Pro Ala Pro Gln Val Glu Ala Val Ala Gln Asp Gln Phe Gln
                165                 170                 175
Gly Ala Ala Arg Ala Trp Met Ala Gly Thr Leu Gln Leu Gly Arg Ala
            180                 185                 190
Leu Arg Pro Arg Gly Leu Trp Gly Phe Tyr Gly Phe Pro Asp Cys Tyr
        195                 200                 205
Asn Tyr Asp Phe Leu Ser Pro Asn Tyr Thr Gly Gln Cys Pro Ser Gly
    210                 215                 220
Ile Arg Ala Gln Asn Asp Gln Leu Gly Trp Leu Trp Gly Gln Ser Arg
225                 230                 235                 240
Ala Leu Tyr Pro Ser Ile Tyr Met Pro Ala Val Leu Glu Gly Thr Gly
                245                 250                 255
Lys Ser Gln Met Tyr Val Gln His Arg Val Ala Glu Ala Phe Arg Val
            260                 265                 270
Ala Val Ala Ala Gly Asp Pro Asn Leu Pro Val Leu Pro Tyr Val Gln
        275                 280                 285
Ile Phe Tyr Asp Thr Thr Asn His Phe Leu Pro Leu Asp Glu Leu Glu
    290                 295                 300
His Ser Leu Gly Glu Ser Ala Ala Gln Gly Ala Ala Gly Val Val Leu
305                 310                 315                 320
Trp Val Ser Trp Glu Asn Thr Arg Thr Lys Glu Ser Cys Gln Ala Ile
                325                 330                 335
Lys Glu Tyr Met Asp Thr Thr Leu Gly Pro Phe Ile Leu Asn Val Thr
            340                 345                 350
Ser Gly Ala Leu Leu Cys Ser Gln Ala Leu Cys Ser Gly His Gly Arg
        355                 360                 365
Cys Val Arg Arg Thr Ser His Pro Lys Ala Leu Leu Leu Leu Asn Pro
    370                 375                 380
Ala Ser Phe Ser Ile Gln Leu Thr Pro Gly Gly Gly Pro Leu Ser Leu
385                 390                 395                 400
Arg Gly Ala Leu Ser Leu Glu Asp Gln Ala Gln Met Ala Val Glu Phe
                405                 410                 415
Lys Cys Arg Cys Tyr Pro Gly Trp Gln Ala Pro Trp Cys Glu Arg Lys
            420                 425                 430
Ser Met Trp
        435
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